

Timothy W. CONNER *et al.*  
Appl. No. 09/540,234  
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## IN THE SPECIFICATION

On page 5, please delete the paragraph spanning lines 16 to 25, and replace it with the following:

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ) ([www-ddbj.nig.ac.jp/](http://www-ddbj.nig.ac.jp/)); Genbank ([www-ncbi.nlm.nih.gov/web/Genbank/Index.html](http://www-ncbi.nlm.nih.gov/web/Genbank/Index.html)); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) ([www-ebi.ac.uk/ebi\\_docs/embl\\_db.html](http://www-ebi.ac.uk/ebi_docs/embl_db.html)). A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designated for nucleotide sequence queries (BLASTN, BLASTX and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology*, 12: 76-80 (1994); Birren, *et al.*, *Genome Analysis*, 1: 543-559 (1997)).

## IN THE CLAIMS:

Please amend the claims as follows:

1. (Twice Amended) A substantially purified nucleic acid molecule that encodes a plant protein or fragment thereof comprising a nucleic acid sequence of SEQ ID NO: 1.